

Claims

What is claimed is:

- 5 1. A method for monitoring differential expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells, comprising:
 - (a) adding a mixture of fluorescence-labeled nucleic acids isolated from the filamentous fungal cells to a substrate containing an array of filamentous fungal ESTs under
10 conditions where the nucleic acids hybridize to complementary sequences of the ESTs in the array, wherein the nucleic acids from the first filamentous fungal cell and the one or more second filamentous fungal cells are labeled with a first fluorescent reporter and one or more different second fluorescent reporters, respectively; and
 - (b) examining the array by fluorescence under fluorescence excitation conditions
15 wherein the relative expression of the genes in the filamentous fungal cells is determined by the observed fluorescence emission color of each spot in the array in which (i) the ESTs in the array that hybridize to the nucleic acids obtained from either the first or the one or more second filamentous fungal cells produce a distinct first fluorescence emission color or one or more second fluorescence emission colors, respectively, and (ii) the ESTs in the array that
20 hybridize to the nucleic acids obtained from both the first and one or more second filamentous fungal cells produce a distinct combined fluorescence emission color.
- 25 2. The method of claim 1, wherein the filamentous fungal ESTs are selected from the group consisting of *Acremonium*, *Aspergillus*, *Fusarium*, *Hemicola*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*, *Thielavia*, *Tolyocladium*, and *Trichoderma* ESTs.
3. The method of claim 2, wherein the filamentous fungal ESTs are *Fusarium* ESTs.
4. The method of claim 3, wherein the filamentous fungal ESTs are *Fusarium*
30 *venenatum* ESTs.
5. The method of claim 4, wherein the *Fusarium venenatum* ESTs are selected from the group consisting of SEQ ID NOs. 1-3770, nucleic acid fragments of SEQ ID NOs. 1-3770, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-3770.

6. The method of claim 5, wherein the *Fusarium venenatum* ESTs are SEQ ID NOs. 1-3770.

5 7. The method of claim 5, wherein the *Fusarium venenatum* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-3770.

8. The method of claim 7, wherein the *Fusarium venenatum* ESTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 1-3770.

10 9. The method of claim 8, wherein the *Fusarium venenatum* ESTs are nucleic acid sequences having at least 99% homology to SEQ ID NOs. 1-3770.

10. The method of claim 9, wherein the *Fusarium venenatum* ESTs are nucleic acid
15 sequences having at least 99.9% homology to SEQ ID NOs. 1-3770.

11. The method of claim 2, wherein the filamentous fungal ESTs are *Aspergillus* ESTs.

12. The method of claim 11, wherein the *Aspergillus* ESTs are *Aspergillus niger* ESTs.

20 13. The method of claim 12, wherein the *Aspergillus niger* ESTs are selected from the group consisting of SEQ ID NOs. 3771-4376, nucleic acid fragments of SEQ ID NOs. 3771-4376, and nucleic acid sequences having at least 90%, preferably at least 95%, more preferably at least 99%, and most preferably at least 99.9% homology to SEQ ID NOs. 3771-
25 4376.

14. The method of claim 13, wherein the *Aspergillus niger* ESTs are SEQ ID NOs. 3771-4376.

30 15. The method of claim 13, wherein the *Aspergillus niger* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 3771-4376.

16. The method of claim 15, wherein the *Aspergillus niger* ESTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 3771-4376.

17. The method of claim 16, wherein the *Aspergillus niger* ESTs are nucleic acid sequences having at least 99% homology to SEQ ID NOs. 3771-4376.

5 18. The method of claim 17, wherein the *Aspergillus niger* ESTs are nucleic acid sequences having at least 99.9% homology to SEQ ID NOs. 3771-4376.

19. The method of claim 11, wherein the *Aspergillus* ESTs are *Aspergillus oryzae* ESTs.

10 20. The method of claim 19, wherein the *Aspergillus oryzae* ESTs are selected from the group consisting of SEQ ID NOs. 4377-7401, nucleic acid fragments of SEQ ID NOs. 4377-7401, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4377-7401.

15 21. The method of claim 20, wherein the *Aspergillus oryzae* ESTs are SEQ ID NOs. 4377-7401.

22. The method of claim 20, wherein the *Aspergillus oryzae* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4377-7401.

20 23. The method of claim 22, wherein the *Aspergillus oryzae* ESTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 4377-7401.

24. The method of claim 23, wherein the *Aspergillus oryzae* ESTs are nucleic acid sequences having at least 99% homology to SEQ ID NOs. 4377-7401.

25 25. The method of claim 24, wherein the *Aspergillus oryzae* ESTs are nucleic acid sequences having at least 99.9% homology to SEQ ID NOs. 4377-7401.

26. The method of claim 2, wherein the filamentous fungal ESTs are *Trichoderma* ESTs.

30 27. The method of claim 26, wherein the filamentous fungal ESTs are *Trichoderma reesei* ESTs.

28. The method of claim 27, wherein the *Trichoderma reesei* ESTs are selected from

the group consisting of SEQ ID NOs. 7402-7860, nucleic acid fragments of SEQ ID NOs. 7402-7860, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 7402-7860.

5 29. The method of claim 28, wherein the *Trichoderma reesei* ESTs are SEQ ID NOs. 7402-7860.

30. The method of claim 28, wherein the *Trichoderma reesei* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 7402-7860.

10 31. The method of claim 30, wherein the *Trichoderma reesei* ESTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 7402-7860.

32. The method of claim 31, wherein the *Trichoderma reesei* ESTs are nucleic acid
15 sequences having at least 99% homology to SEQ ID NOs. 7402-7860.

33. The method of claim 32, wherein the *Trichoderma reesei* ESTs are nucleic acid sequences having at least 99.9% homology to SEQ ID NOs. 7402-7860.

20 34. The method of ~~any of claims 1-33~~, wherein one or more of filamentous fungal cells are selected from the group consisting of an *Acremonium*, *Aspergillus*, *Fusarium*, *Humicola*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*, *Thielavia*, *Tolypocladium*, and *Trichoderma* cell.

25 35. The method of any of claims 1-34, wherein the two or more filamentous fungal cells are the same cell.

36. The method of any of claims 1-35, wherein the two or more filamentous fungal cells are *Fusarium venenatum* cells.

30 37. The method of any of claims 1-35, wherein the two or more filamentous fungal cells are *Aspergillus niger* cells.

38. The method of any of claims 1-35, wherein the two or more filamentous fungal cells

are *Aspergillus oryzae* cells.

39. The method of any of claims 1-34, wherein the two or more filamentous fungal cells are different cells.

40. The method of any of claims 1-39, wherein the hybridization conditions are selected from the group consisting of very low, low, low-medium, medium, medium-high, high, and very high stringency conditions.

41. A computer readable medium having recorded thereon an array of filamentous fungal ESTs for monitoring differential expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells.

42. The computer readable medium of claim 41, wherein the filamentous fungal ESTs are selected from the group consisting of *Acremonium*, *Aspergillus*, *Fusarium*, *Humicola*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*, *Thielavia*, *Tolypocladium*, and *Trichoderma* ESTs.

43. The computer readable medium of claim 42, wherein the filamentous fungal ESTs are *Fusarium* ESTs.

44. The computer readable medium of claim 43, wherein the filamentous fungal ESTs are *Fusarium venenatum* ESTs.

45. The computer readable medium of claim 44, wherein the *Fusarium venenatum* ESTs are selected from the group consisting of SEQ ID NOs. 1-3770, nucleic acid fragments of SEQ ID NOs. 1-3770, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-3770.

46. The computer readable medium of claim 45, wherein the *Fusarium venenatum* ESTs are SEQ ID NOs. 1-3770.

47. The computer readable medium of claim 45, wherein the *Fusarium venenatum* ESTs

are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-3770.

48. The computer readable medium of claim 42, wherein the filamentous fungal ESTs are *Aspergillus* ESTs.

5 49. The computer readable medium of claim 48, wherein the *Aspergillus* ESTs are *Aspergillus niger* ESTs.

50. The computer readable medium of claim 49, wherein the *Aspergillus niger* ESTs are
10 selected from the group consisting of SEQ ID NOs. 3771-4376, nucleic acid fragments of
SEQ ID NOs. 3771-4376, and nucleic acid sequences having at least 90% homology to SEQ
ID NOs. 3771-4376.

51. The computer readable medium of claim 50, wherein the *Aspergillus niger* ESTs are
15 SEQ ID NOs. 3771-4376

52. The computer readable medium of claim 50, wherein the *Aspergillus niger* ESTs are
nucleic acid sequences having at least 90% homology to SEQ ID NOs. 3771-4376.

20 53. The computer readable medium of claim 48, wherein the *Aspergillus* ESTs are
Aspergillus oryzae ESTs.

54. The computer readable medium of claim 53, wherein the *Aspergillus oryzae* ESTs are
selected from the group consisting of SEQ ID NOs. 4377-7401, nucleic acid fragments of
25 SEQ ID NOs. 4377-7401, and nucleic acid sequences having at least 90% homology to SEQ
ID NOs. 4377-7401.

55. The computer readable medium of claim 54, wherein the *Aspergillus niger* ESTs are
SEQ ID NOs. 4377-7401.

30 56. The computer readable medium of claim 54, wherein the *Aspergillus oryzae* ESTs are
nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4377-7401.

57. The computer readable medium of claim 42, wherein the filamentous fungal ESTs are

Trichoderma ESTs.

58. The computer readable medium of claim 57, wherein the filamentous fungal ESTs are *Trichoderma reesei* ESTs.

59. The computer readable medium of claim 58, wherein the *Trichoderma reesei* ESTs are selected from the group consisting of SEQ ID NOs. 7402-7860, nucleic acid fragments of SEQ ID NOs. 7402-7860, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 7402-7860.

60. The computer readable medium of claim 59, wherein the *Trichoderma reesei* ESTs are SEQ ID NOs. 7402-7860.

61. The computer readable medium of claim 59, wherein the *Trichoderma reesei* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 7402-7860.

62. The computer readable medium of any of claims 41-61, wherein the medium is selected from the group consisting of a floppy disk, a hard disk, random access memory (RAM), read only memory (ROM), and CD-ROM.

63. A computer-based system for monitoring differential expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells comprising the following elements:

(a) a data storage means comprising filamentous fungal ESTs selected from the group consisting of SEQ ID NOs. 1-7860, nucleic acid fragments of SEQ ID NOs. 1-7860, and nucleic acid sequences having at least 90% homology to the sequences of SEQ ID NOs. 1-7860;

(b) a search means for comparing a target sequence to a filamentous fungal EST sequence of the data storage means of step (a) to identify homologous sequences; and

(c) a retrieval means for obtaining the homologous sequence(s) of step (b).

64. A substrate comprising an array of filamentous fungal ESTs for monitoring differential expression of a plurality of genes in a first filamentous fungal cell relative to

expression of the same genes in one or more second filamentous fungal cells.

65. The substrate of claim 64, wherein the filamentous fungal ESTs are selected from the group consisting of *Acremonium*, *Aspergillus*, *Fusarium*, *Humicola*, *Mucor*, *Myceliophthora*,
5 *Neurospora*, *Penicillium*, *Thielavia*, *Tolypocladium*, and *Trichoderma* ESTs.

66. The substrate of claim 65, wherein the filamentous fungal ESTs are *Fusarium* ESTs.

67. The substrate of claim 66, wherein the filamentous fungal ESTs are *Fusarium*
10 *venenatum* ESTs.

68. The substrate of claim 67, wherein the *Fusarium venenatum* ESTs are selected from the group consisting of SEQ ID NOs. 1-3770, nucleic acid fragments of SEQ ID NOs. 1-3770, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-3770.

15 69. The substrate of claim 68, wherein the *Fusarium venenatum* ESTs are SEQ ID NOs. 1-3770.

70. The substrate of claim 68, wherein the *Fusarium venenatum* ESTs are nucleic acid
20 sequences having at least 90% homology to SEQ ID NOs. 1-3770.

71. The substrate of claim 65, wherein the filamentous fungal ESTs are *Aspergillus* ESTs.

72. The substrate of claim 71, wherein the *Aspergillus* ESTs are *Aspergillus niger* ESTs.

25 73. The substrate of claim 72, wherein the *Aspergillus niger* ESTs are selected from the group consisting of SEQ ID NOs. 3771-4376, nucleic acid fragments of SEQ ID NOs. 3771-4376, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 3771-4376.

30 74. The substrate of claim 73, wherein the *Aspergillus niger* ESTs are SEQ ID NOs. 3771-4376

75. The substrate of claim 73, wherein the *Aspergillus niger* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 3771-4376.

76. The substrate of claim 71, wherein the *Aspergillus* ESTs are *Aspergillus oryzae* ESTs.

77. The substrate of claim 76, wherein the *Aspergillus oryzae* ESTs are selected from the group consisting of SEQ ID NOs. 4377-7401, nucleic acid fragments of SEQ ID NOs. 4377-7401, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4377-7401.

78. The substrate of claim 77, wherein the *Aspergillus niger* ESTs are SEQ ID NOs. 4377-7401.

79. The substrate of claim 77, wherein the *Aspergillus oryzae* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4377-7401.

80. The substrate of claim 65, wherein the filamentous fungal ESTs are *Trichoderma* ESTs.

81. The substrate of claim 80, wherein the filamentous fungal ESTs are *Trichoderma reesei* ESTs.

82. The substrate of claim 81, wherein the *Trichoderma reesei* ESTs are selected from the group consisting of SEQ ID NOs. 7402-7860, nucleic acid fragments of SEQ ID NOs. 7402-7860, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 7402-7860.

83. The substrate of claim 82, wherein the *Trichoderma reesei* ESTs are SEQ ID NOs. 7402-7860.

84. The substrate of claim 82, wherein the *Trichoderma reesei* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 7402-7860.

85. An isolated nucleic acid sequence comprising any of SEQ ID NOs. 1-7860.

86. The nucleic acid sequence of claim 85, wherein SEQ ID NOs. 1-3770 are obtained from *Fusarium venenatum*.

87. The nucleic acid sequence of claim 85, wherein SEQ ID NOs. 3771-4376 are obtained from *Aspergillus niger*.

5 88. The nucleic acid sequence of claim 85, wherein SEQ ID NOs. 4377-7401 are obtained from *Aspergillus oryzae*.

89. The nucleic acid sequence of claim 85, wherein SEQ ID NOs. 7402-7860 are obtained from *Trichoderma reesei*.

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